

 PALM IntranetApplication
Number

IDS Flag Clearance for Application 10607834

IDS
Information

Content	Mailroom Date	Entry Number	IDS Review	Last Modified	Reviewer
M844	2004-07-16	18	Y <input checked="" type="checkbox"/>	2004-08-06 12:04:18.0	lbanks1
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UniProtKB/TrEMBL entry Q8XDC9


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[\[Keywords\]](#) [\[Features\]](#) [\[Sequence\]](#) [\[Tools\]](#)


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Entry information

Entry name	Q8XDC9_ECO57
Primary accession number	Q8XDC9
Secondary accession number	Q7AG40
Integrated into TrEMBL on	March 1, 2002
Sequence was last modified on	March 1, 2002 (Sequence version 1)
Annotations were last modified on	February 6, 2007 (Entry version 33)
Name and origin of the protein	
Protein name	Homolog of Salmonella FimH protein
Synonyms	None
Gene name	OrderedLocusNames: ECs1025, Z1290
From	Escherichia coli O157:H7 [TaxID: 83334] [HAMAP prote
Taxonomy	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.

References

- [1] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
 DOI=10.1038/35054089; PubMed=11206551 [NCBI, ExPASy, EBI, Israel, Japan]
 Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Ev
 P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller
 Grotbeck E.J., Davis N.W., Lim A., , Blattner F.R.;
 "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
 Nature 409:529-533(2001).
- [2] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=O157:H7 / Sakai / RIMD 0509952 / EHEC;
 DOI=10.1093/dnares/8.1.11; PubMed=11258796 [NCBI, ExPASy, EBI, Israel, Japan]
 Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsu
 Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C.

Ogasawara N., Yasunaga T., Kuhara S., , Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001).

Comments

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Cross-references

Sequence databases

EMBL	AE005174; AAG55427.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
	BA000007; BAB34448.1; -; Genomic_DNA.	[EMBL / GenBank / DDBJ] [CoDingSequence]
PIR	A99757; A99757. G85620; G85620.	

3D structure databases

ModBase Q8XDC9.

Enzyme and pathway databases

BioCyc ECOL83334-1:ECS1025-MONOMER; -.

Organism-specific gene databases

HOGENOM [Family / Alignment / Tree]

Family and domain databases

InterPro	IPR008966; Adhes_bact. IPR000259; Fimbrial. Graphical view of domain structure.
Gene3D	G3DSA:2.60.40.1090; Fimbrial; 1.
ProDom	[Domain structure / List of seq. sharing at least 1 domain]

Genome annotation databases

GenomeReviews	BA000007_GR; ECs1025. AE005174_GR; Z1290.
KEGG	ece:Z1290; -. ecs:ECs1025; -.
CMR	Q8XDC9; Z1290.

Other

UniRef View cluster of proteins with at least 50% / 90% / 100% identity.

Keywords

Complete proteome.

Features

None

Sequence information

Length: 326 Molecular weight: 34628 CRC64: 5CB08328B5C23573 [This is a checksum o
AA Da sequence]

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      10      20      30      40      50      60
MQIIFGEKCV SLLRLFFAAV LMLWCAQTAA YSGQCHTTQG NPYIGVNFGV KTLLEEENTT

      70      80      90     100     110     120
GVVKDKFYQW NESNDYYVSC DCDKDNVRSR RWAFAADSPL VYLGDNWKI NDYLAQVLL

     130     140     150     160     170     180
QVKGSSPTAV PFENVGTGAD TRWHICDPGG QRLGGQGASG NSGSFSLKIL QPFVGSVIP

     190     200     210     220     230     240
PMALARLFEC YNIPAGDSCT TTGTPVLVYY LSGTINSLGS CSVNAGETIE VDLGDFVFAAN

     250     260     270     280     290     300
FRVVGHKPLG ARTAELAIPV RCNTGNAGLV NVNLSLTATT DPSYPQAIKT SRPGVGVVVT

     310     320
DSQNNIISPA GGTLPISIPD DADSIA

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Sequence analysis tools: ProtParam,
ProtScale, Compute pI/Mw, PeptideMass,
PeptideCutter, Dotlet (Java)



ScanProsite, MotifScan



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analysis tools



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